

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 03:30:16 ; Search time 5816 Seconds  
(without alignments)

16683.073 Million cell updates/sec

Title: US-10-046-433-39

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Perfect score: 100%
Sequence: 1 gcaagaagcagcgcgcagc.....attaaaaaaaaaaaaaa 3334

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Scoring table:	IDENTITY_NUC	Canext
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3303.4	99.1	3501	6	AX463904	AX463904 Sequence
2	3259.6	97.8	3280	6	AX036667	AX036667 Sequence
3	3258.8	97.7	3331	6	AX127726	AX127726 Sequence
4	2726.6	81.8	2733	6	AX127740	AX127740 Sequence
5	2603.6	78.1	2610	6	AX127742	AX127742 Sequence
6	2603	78.1	2895	9	AK057647	AK057647 Homo sapi
7	2227	66.8	2449	9	BC031648	BC031648 Homo sapi
8	2094.4	62.8	2129	9	AK026892	AK026892 Homo sapi
9	1938	58.1	5567	9	AB037745	AB037745 Homo sapi
10	1705	51.1	1717	6	AX013071	AX013071 Sequence
11	1145.8	34.4	1149	6	AX127746	AX127746 Sequence
12	1008.8	30.3	1587	6	AX123277	AX123277 Sequence
13	951.8	28.5	1119	6	AX213279	AX213279 Sequence
14	834.4	25.0	1149	10	BC022655	BC022655 Mus muscu
15	807.8	24.2	3185	9	AK055902	AK055902 Homo sapi
16	641.4	19.8	627	6	AX036669	AX036669 Sequence
17	625.4	18.2	677	6	AX127744	AX127744 Sequence
18	537.6	16.1	1737	6	AX060311	AX060311 Sequence
19	443	13.3	443	6	AX127734	AX127734 Sequence
20	424.4	12.7	426	6	AX368203	AX368203 Sequence
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22	399	12.0	480	6	AX182004	AX182004 Sequence
23	382.6	11.5	437	6	AX182039	AX182039 Sequence
24	346	10.4	373	6	AX070263	AX070263 Sequence
25	343.4	10.3	353	6	AX182022	AX182022 Sequence
26	337.2	10.1	399	6	AX182000	AX182000 Sequence
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28	292.2	8.8	116603	3	AX261103	AX261103 Sequence
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38	210	6.3	146536	2	AC011645	AC011645 Homo sapi
39	208.4	6.3	45857	2	AL138933	AL138933 Human DN
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41	189.6	5.7	171	6	AX302725	AX302725 Sequence
42	162.8	4.9	171	6	AX127730	AX127730 Sequence
43	162.8	4.9	404	6	AX071721	AX071721 Sequence
44	162	4.9	164800	6	AC113756	AC113756 Rattus no
45	158	4.7	158	6	AX127732	AX127732 Sequence

## ALIGNMENTS

RESULT 1	AX463904	3501 bp	DNA	linear	PAT 16-JUL-2002
LOCUS	AX463904				
DEFINITION	Sequence 37 from Patent WO0140466.				
ACCESSION	AX463904				
VERSION	AX463904.1	GT:21898969			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE  
AUTHORS  
1  
Baker, K. P., Beresini, M., DeForge, L., Desnoyers, L., Pillaroff, E.,  
Gao, W. O., Gerlitsen, M. E., Goddard, A., Godowski, P. J., Gurney, A. L.,  
Sherwood, S., Smith, V., Stewart, T. A., Tunas, D., Watanabe, C. K.,



Db 1996 CCCCCTAACACAAATTCGAAAGCCACAGCCTTATGGTCTCCAGGCGCTGTGCTCCGT  
 Qy 1991 GGTCCAGGAGCCAGACACAGATCCTCTGTGTCTACATGATTCACCTCTCA 2040  
 Db 2056 GGTCCAGGAGCCAGACACAGATCCTCTGTGTCTACATGATTCACCTCTCA 2115  
 Qy 2041 GCGAACATCCACAGAGACTTTCACATCAACCTCTCCGCTTTGGCAACACCTCACT 2100  
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RESULT 2  
 AX036667 3280 bp DNA linear PAT 16-NOV-2000  
 LOCUS Sequence 1 from Patent WO058460.  
 DEFINITION AX036667  
 ACCESSION AX036667  
 VERSION AX036667.1 GI:11226242  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 human.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 1 (bases 1 to 3280)  
 Bruck,C.E., Vinals,Y.D., Coche,T. and Cassart,J.P.  
 Novel compounds  
 Patent: WO 0058460-A 1 05-OCT-2000;  
 JOURNAL BRUCK CLAUDE ELVIRE MARIE (BE) ; SMITHKLINE BEECHAM BIOLOG (BE) ;  
 VINALS Y DE BASOLS CARLOTTA (BE) ; COCHE THIERRY (BE) ; CASSART  
 JEAN POL (BE)  
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 location/Qualifiers  
 source  
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 /db\_xref="taxon:9606"  
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 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 3273; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
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 Qy 118 GCGATATCCCGGCTGTGGCGGCTGTGCTGTGGCTGTGGACGCGCTTCCAGTGAACCCAG 177  
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 Db 121 GGAAGGAGACCGAGCTTACGCTGTGCAAGAGTCTAGTACACATGATGATGATGATGATGATGATGAT 180  
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 Db 241 AGCTGCTGATACCCGCTCAAGGACCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
 Qy 358 CTGATATGAAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417

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QY 2446 TTCTTTTATAGTCCAAATGATGATGACCCAGTCTGCAAGTTTGGGAATGCAACCAATC 2505  
Db 2433 TTCTTTTATAGTCCAAATGATGATGACCCAGTCTGCAAGTTTGGGAATGCAACCAATC 2492  
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Db 2493 CCGCTCAGGTGCACTCCACAGAAACTGTCCCTGGAAGTTTGTCTGCGCAGGAACGTGC 2552  
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Query Match		78.1%;	Score 2603.6; DB 6; Length 2610;
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Matches 2606; Conservative		0; Mismatches	4; Indels 0; Gaps 0;
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DB	61	GACAGCAGGGGTTCCAGGTGAGGGTCCGCTGCCGATACCCGGGCGTGTGACACAGC	120
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DB	121	CTGCGTCAACCCGCTGAAGGCGACAGTGTCTCTCTCTGCAACGCCGGGGAAGTTTGTG	180
QY	361	GATATGAAGGACGACGATGTAAAGCATGCGCTGAGGGCGGCTACTCTCTGCGACAGGC	420
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DB	361	CGGGGCGACTACATCGCTTCAACAGGAGATGACAGCCACACTGATGTACGCCGCTC	420
QY	601	AACCTGAGCATCTGGCACCGTTAACTTGAATACTACTATCCAGACTCCAGCATCATC	660
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DB	481	TTTGGATTTTGTGTCAGATGACGTCGACGCCCAATGAGAGTACTCCAGGTGATG	540
QY	721	AAGACCAAGAGAAAGATGGAATTCACAGTGTGAGCTAAATGAGGCAATAATGTC	780
DB	541	AAGACCAAGAGAAAGATGGAATTCACAGTGTGAGCTAAATGAGGCAATAATGTC	600
QY	781	CTGTATTTGGGAACACAGGCTTCTAGATGACCAAAAGTACCCAAAGCTGTGCTG	840
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DB	661	AGAAACATTTGCAATACAGGGGTGGCTTACACTTCAAGATGCTTCCCTGCAAACTGGC	720
QY	901	ACGTATGACAGCAAGGCTCTCTTCTGCAAACTTTCGCCAGCAACTTATATCA	960
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QY	1021	TCTTCTGTAGCTGGGCGGCTGTGACAGCAAGAAATATTTTACACACAGCGGC	1080
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QY	1081	TGCGATGCCAACGGAGAGACACAACTCATGTATACAAATGGGCCAAGCGAAATCTGTAC	1140
DB	901	TGCGATGCCAACGGAGAGACACAACTCATGTATACAAATGGGCCAAGCGAAATCTGTAC	960
QY	1141	GAGGACCTTGAAGGGGCGAGTGAAGCTGCTCTGTGTGTGAAGACCACTGCCACCC	1200
DB	961	GAGGACCTTGAAGGGGCGAGTGAAGCTGCTCTGTGTGTGAAGACCACTGCCACCC	1020
QY	1201	TGCAACCCAGGCTTCTTCAAAACCAACACAGCAGCTGCCAGCCCTGACATATGTTCC	1260
DB	1021	TGCAACCCAGGCTTCTTCAAAACCAACACAGCAGCTGCCAGCCCTGACATATGTTCC	1080
QY	1261	TACTCCAAATGAGGCTTACACCTGACCTGCTGCTGACAGGACTGAACCTGCTGTGGATTT	1320
DB	1081	TACTCCAAATGAGGCTTACACCTGACCTGCTGCTGACAGGACTGAACCTGCTGTGGATTT	1140
QY	1321	GAATACAAATGTGGGAGACAGCTGCGCCCAACAAATGGAAGACCGTTTCAGTGGGATC	1380
DB	1141	GAATACAAATGTGGGAGACAGCTGCGCCCAACAAATGGAAGACCGTTTCAGTGGGATC	1200
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DB	1201	AACCTGAGTACAAAGGCGATGACAGGCTGGGAGGTGGCTGGTATCATATTTACACAGT	1260
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DB	1261	GCTGAGGCTTACAGCAATGACTTATATTTCTACTCTGTGTGTGCGAGGATTTAGACT	1320
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DB	1321	CCGAGTGGGTGATGGGAGACACAGAGATTAAGAGTGGCGCAATCAATTTGCTTT	1380
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DB	1381	GAGACCTCTGTGTGTGAACCTGTGACCTTACTTCAATGTGGGTGGAATTTAGAGAC	1440
QY	1621	AACACTCTGTGTGAGAGCTGGAAGGTTCCAAAGGCAAAACAGTCTTATACCTATCATTT	1680
DB	1441	AACACTCTGTGTGAGAGCTGGAAGGTTCCAAAGGCAAAACAGTCTTATACCTATCATTT	1500
QY	1681	GAGGAGAACACTTACACAGAGCTTCACTGGGCTTCCAGAGGACACTTTTCATAGAGCA	1740
DB	1501	GAGGAGAACACTTACACAGAGCTTCACTGGGCTTCCAGAGGACACTTTTCATAGAGCA	1560
QY	1741	AGCAGGAAGTACCAATGACGTTGCCAAGATCTACTCATCAATGTTCACCAATGTTATG	1800
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QY	1801	AATGGCGTGGCTCTTACTGCGTCCGTCGTCAGAGGCTGTCGATGTGGGTCTCTCC	1860
DB	1621	AATGGCGTGGCTCTTACTGCGTCCGTCGTCAGAGGCTGTCGATGTGGGTCTCTCC	1680
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DB	1681	TGCACCTTGTCTGCTGTGTACTATATTTAGCCAGATTCAGAACCTGCGACTCTCCG	1740
QY	1921	CCCCCTAACCAATTTCTAAAGCCACAGCCTTATGGTGTTCAGGCTGTGTGCTCTGT	1980
DB	1741	CCCCCTAACCAATTTCTAAAGCCACAGCCTTATGGTGTTCAGGCTGTGTGCTCTGT	1800
QY	1981	GSTCAGGAGCAAGAACAAAGATTCAGTCTGTGCTCAATGATGATGACCTTCTCA	2040

DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
Db	1801	GGTCCAGGGAGCCAAAGAACCAACAGATCCACTCTCTGTCTACAAATGATTCGACCTTCTCA	1860						
QY	2041	CGGAACACTTCAACACGAGACTTTCACCTACACACTTCTCCGCTTTGGCAACACCGTCACT	2100						
Db	1861	CGCAACACTTCAACACGAGACTTTCACCTACACACTTCTCCGCTTTGGCAACACCGTCACT	1920						
QY	2101	CTTGTCTGAGGGGCAAGCTTCACCTCCAAAGGGGTGAATACCTTCCATGCATTTACCTTC	2160						
Db	1921	CTTGTCTGAGGGGCAAGCTTCACCTCCAAAGGGGTGAATACCTTCCATGCATTTACCTTC	1980						
QY	2161	AGTCTCTGTGAAACCAAGGCTAGGAAATGTCTGTGTGACCCACCAATGTCACTGTGACTTC	2220						
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QY	2221	CGGATTCCTGAGGGGTGAGTCAAGGTTCTCCAAATCTATATCAACAGCTTACCTGTCTCCAGGCA	2280						
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QY	2281	GTCATATATCCCTCCAGAGGTGACAGGCTACAAAGCCGGGGTTTCCTACAGCTGTACAGC	2340						
Db	2101	GTCATATATCCCTCCAGAGGTGACAGGCTACAAAGCCGGGGTTTCCTACAGCTGTACAGC	2160						
QY	2341	CTTGTCTGATGCACTTATTTGAGGGTGAACAACAGATATCACTTGGATGGAATCACTCTCCCA	2400						
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QY	2401	GCTGAACCTTTTCCACCTGTGAGTCTTTGGGAATACCGAGCTGATCTTCTTTTATAGGTCC	2460						
Db	2221	GCTGAACCTTTTCCACCTGTGAGTCTTTGGGAATACCGAGCTGATCTTCTTTTATAGGTCC	2280						
QY	2461	AATGATGTATACCCAGTCTCTGACACTTCTGGGAGATCAACCACTCCGCGTCAAGTCTCACT	2520						
Db	2281	AATGATGTATACCCAGTCTCTGACACTTCTGGGAGATCAACCACTCCGCGTCAAGTCTCACT	2340						
QY	2521	CCACAGAAAACCTGTCCCTGGAAGTTGTCTGTCTCCAGGAACGCTCAGATGGGAGACTGT	2580						
Db	2341	CCACAGAAAACCTGTCCCTGGAAGTTGTCTGTCTCCAGGAACGCTCAGATGGGAGACTGT	2400						
QY	2581	GATGCTGCACTTCCACTTCTCTGTGGAGAGCGCGCTTGTGCCCGCTCTGCTCAAGTG	2640						
Db	2401	GATGCTGCACTTCCACTTCTCTGTGGAGAGCGCGCTTGTGCCCGCTCTGCTCAAGTG	2460						
QY	2641	GCTGATACCTGATGTCTCTGTCAGACACTGTGTGGGCTGGGATCTCAGAAAGCTACTTACGTG	2700						
Db	2461	GCTGATACCTGATGTCTCTGTCAGACACTGTGTGGGCTGGGATCTCAGAAAGCTACTTACGTG	2520						
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LOCUS	AK057647	2895 bp mRNA linear PRI 01-AUG-2002							
DEFINITION	AK057647	Homo sapiens CDNA FLJ33085 fis. clone TRACH2000420, weakly similar to MAJOR SURFACE LABELLED TROPHOZOITE ANTIGEN PRECURSOR.							
ACCESSION	AK057647	AK057647.1 GI:16553406							
KEYWORDS	AK057647	oligo capping; fis (full insert sequence).							
VERSION	AK057647	Homo sapiens trachea cDNA to mRNA, clone_1lb:TRACH2							
SOURCE	AK057647	clone:TRACH2000420.							
ORGANISM	AK057647	Homo sapiens							
REFERENCE	AK057647	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	AK057647	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
	1	Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,							
		Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,							
		Yoshikawa, Y., Matsumura, Y., Moriya, S., Chida, E., Momiyama, H.,							
		Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E.,							

TITLE	JOURNAL	REFERENCE	AUTHORS	JOURNAL	TITLE
NEO human cDNA sequencing project	Unpublished	2 (bases 1 to 2895)	Isogai,T., Otsuki,T. and Sugiyama,T.		
Direct Submission	Submitted (24-Oct-2001)	Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)			
NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- and 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center; National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.					
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					Gaps 1;
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QY	121	ATACCCGGCGCTGTGGCGGCTCTGCTCTGGGCTGGAGCCGCTTTCAGAGTACCCAGGGA	180		
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QY	181	ACGGGACGGGCGTTCACCGCTCGCAAGAGTGTAGTACCACTATAGGTACACGGCGTGT	240		
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QY	241	GACAGCAGCGGTTTCAGGTGAGGGGTGGCCCTGCGCATATACCCGGGCGCTTGCACAGC	300		
DB	263	GACAGCAGCGGTTTCAGGTGAGGGGTGGCCCTGCGCATATACCCGGGCGCTTGCACAGC	322		
QY	301	CTGCGTACCCCGTTCANAGGCGACCGAGTCTCTTCTCTGCAACGCCGGGGAGTTTCTG	360		
DB	323	CTGCGTACCCCGTTCANAGGCGACCGAGTCTCTTCTCTGCAACGCCGGGGAGTTTCTG	382		
QY	361	GATATGAAGGACCGATATGTAACCATGAGCGCTAGAGGCGGCTACTCCCTGGGACAGGC	420		
DB	383	GATATGAAGGACCGATATGTAACCATGAGCGCTAGAGGCGGCTACTCCCTGGGACAGGC	442		
QY	421	ATTGCGTTTGTATGATGGGATAGACTCCCATGGCTTTGGCAGACCTCTCAGCCAAATG	480		
DB	443	ATTGCGTTTGTATGATGGGATAGACTCCCATGGCTTTGGCAGACCTCTCAGCCAAATG	502		
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RESULT 7	
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LOCUS	BC031648
DEFINITION	2449 bp mRNA linear PRJ 26-JUN-2007
ACCESSION	Homo sapiens, K1A1324 protein, clone MGC:35166 IMAGE:5169952,
VERSION	BC031648
KEYWORDS	BC031648.1 GI:21594947
SOURCE	MGC.
ORGANISM	human.
	Homo sapiens

REMARK COMMENT	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huilyk, S.W., Hale, S.M.,  
 Yoon, V.S., Kovals, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/INTL at: <http://image.lnl.gov>  
Series: IRAK Plate: 51 Row: d Column: 23  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES	Location/Qualifiers
source	1. .2449

**CDS**

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2238; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 377 ACTGACCCGCTGCCTGCAGGGGACTGAACCTGCTGGGATTTGATATACAAATGTTGCA 1336

QY 1337 ACACGCTGCCACCAACATGGAAGACGCGCTTCTCAGTGGATCACTTCAGTACAAG 1396

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[illegible]

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QY	3076	GAGGCCAGACATGAGACCTGTGAGAGGACATCGCTGCTCACCCTGCCTCCACTTCCA	3135
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QY	3136	TAGCACCTTTCAGAGCCTGCGGGCGATTGGGTGCCAGATCCGCAACGCCACATGCTGG	3195
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QY	3196	AAATCTCTTCATGTGGCGCTTATCAGATGTTTGAATTCAGATCTTTTATATAGATAC	3255
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QY	3256	CCAAACCCCTCTTCTGCTGCTTCCAAACCTGCCAAATATATCCACACCTTTGTTGTAA	3315
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LOCUS	AK026832		
DEFINITION	Homo sapiens CDNA: FLJ23179 fls, clone LNG10890.		
ACCESSION	AK026832.1	GI:10439779	
VERSION	AK026832.1	GI:10439779	
KEYWORDS	oligo capping; fls (full insert sequence).		
SOURCE	Homo sapiens human lung CDNA to mRNA, clone_l1b:LNG clone:LNG10890.		
ORGANISM	Homo sapiens		
REFERENCE	Ekabayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (slices)		
	Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsunuma,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hiroo,M., Ohmori,Y., Ota,T., Suzuki,Y., Odayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 2129)		
AUTHORS	Sugano,S., Suzuki,Y., Ota,T., Odayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan (E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)		
COMMENT	NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by science and technology Agency).		
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Matches 2109; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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 REFERENCE 1 (sites)  
 AUTHORS Nagase, T., Kikuno, R., Ishikawa, K. I., Hirosewa, M. and Ohara, O.  
 TITLE Prediction of the coding sequences of unidentified human genes.  
 XVI. The complete sequences of 150 new cDNA clones from brain which  
 code for large proteins in vitro  
 JOURNAL DNA Res. 7 (1), 65-73 (2000)  
 MEDLINE 2 (bases 1 to 5567)  
 REFERENCE Ohara, O., Nagase, T. and Kikuno, R.  
 AUTHORS Direct Submission  
 JOURNAL Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,  
 Laboratory of DNA Technology, 1532-3 Yana, Kisarazu, Chiba  
 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,  
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AUTHORS	1 (bases 1 to 1149)		
TITLE	Delneste, Y., Magistrelli, G., Jeannin, P. and Bonnefoy, J.Y.		
JOURNAL	Cloning, expression and characterisation of a gene expressed in tumour cells and involved in the regulation of the immune response		
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FEATURES	source
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REFERENCE	Homo sapiens
AUTHORS	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
TITLE	Tashiro, H., Yamazaki, M., Watanabe, K., Kunagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiya, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagaatsuma, M., Murakawa, K., Kanehori, K., Takahashi, Fujii, A., Oshimari, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagaishi, K., Masuno, Y., Nagai, K. and Isogai, T.
JOURNAL	NEDO human cDNA sequencing project
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 3185)
TITLE	Isogai, T., Otsuki, T. and Sugiyama, T.
JOURNAL	Direct Submission
COMMENT	Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library construction: Helix Research Institute (RAB) (supported by Japan Key Technology Center etc.); 5'-6' end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.
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